Resource Summary Report

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HPRD - Human Protein Reference Database

RRID:SCR_007027
Type: Tool

Proper Citation

HPRD - Human Protein Reference Database (RRID:SCR_007027)

Resource Information

URL: http://www.hprd.org

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Description: Database that represents a centralized platform to visually depict and integrate information pertaining to domain architecture, post-translational modifications, interaction networks and disease association for each protein in the human proteome. All the information in HPRD has been manually extracted from the literature by expert biologists who read, interpret and analyze the published data.

Abbreviations: HPRD

Synonyms: Human Protein Reference Database

Resource Type: data or information resource, database

Defining Citation: PMID:18988627, PMID:16381900, PMID:14525934

Keywords: protein, disease, network, post-translational, proteome, protein binding, protein s, protein c, pathway, protein-protein interaction, protein expression, subcellular localization, phosphorylation motif, signaling pathway, protein sequence, blast, molecule, domain, motif, post-translational modification, protein isoform, FASEB list

Funding:

Availability: Acknowledgement requested, Free, Non-commercial, Commercial requires license

Resource Name: HPRD - Human Protein Reference Database

Resource ID: SCR_007027

Alternate IDs: nif-0000-00137

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250507T060446+0000

Ratings and Alerts

No rating or validation information has been found for HPRD - Human Protein Reference Database.

No alerts have been found for HPRD - Human Protein Reference Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1237 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Wright SN, et al. (2025) State of the interactomes: an evaluation of molecular networks for generating biological insights. Molecular systems biology, 21(1), 1.

Zhai Y, et al. (2025) Network pharmacology: a crucial approach in traditional Chinese medicine research. Chinese medicine, 20(1), 8.

Ni T, et al. (2025) Integrated Transcriptome Analysis Reveals Novel Molecular Signatures for Schizophrenia Characterization. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(2), e2407628.

Yang G, et al. (2025) DTI-MHAPR: optimized drug-target interaction prediction via PCA-enhanced features and heterogeneous graph attention networks. BMC bioinformatics, 26(1), 11.

Sun L, et al. (2025) ISLRWR: A network diffusion algorithm for drug-target interactions prediction. PloS one, 20(1), e0302281.

Kiouri DP, et al. (2025) Structure-Based Approaches for Protein-Protein Interaction Prediction Using Machine Learning and Deep Learning. Biomolecules, 15(1).

Cabello AL, et al. (2024) Brucella-driven host N-glycome remodeling controls infection. Cell

host & microbe, 32(4), 588.

Lai W, et al. (2024) Integrated analysis of scRNA-seq and bulk RNA-seq identifies FBXO2 as a candidate biomarker associated with chemoresistance in HGSOC. Heliyon, 10(7), e28490.

Bernett J, et al. (2024) Cracking the black box of deep sequence-based protein-protein interaction prediction. Briefings in bioinformatics, 25(2).

Csabai L, et al. (2024) AutophagyNet: high-resolution data source for the analysis of autophagy and its regulation. Autophagy, 20(1), 188.

Hu C, et al. (2024) Optimizing drug combination and mechanism analysis based on risk pathway crosstalk in pan cancer. Scientific data, 11(1), 74.

Xie Y, et al. (2024) Network Analysis of Osteoarthritis Progression Using a Steiner Minimal Tree Algorithm. Journal of inflammation research, 17, 3201.

Tian J, et al. (2024) The Impact of the COVID-19 Pandemic on Staffing Levels in Philadelphia Nursing Homes: Disparities Based on the Racial Composition of Geographical Areas. Policy, politics & nursing practice, 25(3), 152.

Liu L, et al. (2024) Kinesin Family Member C1: Function in liver hepatocellular carcinoma and potential target for chemotherapeutic. Heliyon, 10(18), e37832.

Murdoch E, et al. (2024) Hypothesis: evidence that the PRS gene products of Saccharomyces cerevisiae support both PRPP synthesis and maintenance of cell wall integrity. Current genetics, 70(1), 6.

Simhal AK, et al. (2024) High WEE1 expression is independently linked to poor survival in multiple myeloma. bioRxiv : the preprint server for biology.

Alberuni S, et al. (2024) Integration of biological data via NMF for identification of human disease-associated gene modules through multi-label classification. PloS one, 19(12), e0305503.

Gou Y, et al. (2024) GPS-SUMO 2.0: an updated online service for the prediction of SUMOylation sites and SUMO-interacting motifs. Nucleic acids research, 52(W1), W238.

Wang H, et al. (2024) Interpretable deep learning methods for multiview learning. BMC bioinformatics, 25(1), 69.

Zorn P, et al. (2024) Rbfox1 controls alternative splicing of focal adhesion genes in cardiac muscle cells. Journal of molecular cell biology, 16(1).